



## SEQUENCE LISTING

RECEIVED

NOV 01 2002

EPO 01/02

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\*111\*

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\*114\* US 09/661,992

\*115\* 106

\*117\* PatentIn Ver. 2.1

\*118\* 1

\*119\* 26

\*120\* DNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 1

gtcaattttc ttgtccacct tgggtgc

26

\*116\* 1

\*117\* 26

\*118\* DNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 2

ctcgattctc ttgatcaact cagtct

26

\*110\* 3

\*111\* 34

\*112\* DNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 3

ttgaatgggc acatgcagat ctct

24

\*110\* 4

\*111\* 34

\*112\* DNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 4

ctcattcttg ttgaagctct tgac

24

<210> 5  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 5  
Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr  
1 5 10

<211> 6  
<212> 12  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 6  
Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr  
1 5 10

<211> 7  
<212> 13  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 7  
Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val  
1 5 10

<211> 8  
<212> 13  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 8  
Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val  
1 5 10

<211> 9  
<212> 13  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 9

Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val  
1 5 10

4110 10  
4111 13  
4112 PPT  
4113 Artificial Sequence

4120  
4123 Description of the artificial sequence:CDR3 region

4130 10  
Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr  
1 5 10

4140 11  
4141 16  
4142 PPT  
4143 Artificial Sequence

4150  
4153 Description of the artificial sequence:CDR3 region

4160 13  
Glu Glu Glu Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu  
1 5 10 15

Glu Glu

4170 12  
4171 18  
4172 PPT  
4173 Artificial Sequence

4180  
4183 Description of the artificial sequence:CDR3 region

4190 13  
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4200 13  
4201 18  
4202 PPT  
4203 Artificial Sequence

4210  
4213 Description of the artificial sequence:CDR3 region

4220 13  
Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu  
1 5 10 15

Trp Glu

<210> 14  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 14  
Val Arg Tyr Arg Asn Arg Tyr Arg Trp Gly Tyr Arg Gly Arg Phe Gly  
1 5 10 15

Asp Glu

<210> 15  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 15  
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg  
1 5 10 15

Arg Arg

<210> 16  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 16  
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 17  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 17  
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg  
1 5 10 15

Arg Arg

Q2100: 18  
Q2110: 18  
Q2120: PRT  
Q2130: Artificial Sequence

Q2200:  
Q2230: Description of the artificial sequence:CDR3 region

Q4000: 18  
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

Q2100: 19  
Q2110: 18  
Q2120: PRT  
Q2130: Artificial Sequence

Q2200:  
Q2230: Description of the artificial sequence:CDR3 region

Q4000: 19  
Arg Arg Arg Ala Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

Q2100: 20  
Q2110: 18  
Q2120: PRT  
Q2130: Artificial Sequence

Q2200:  
Q2230: Description of the artificial sequence:CDR3 region

Q4000: 20  
Arg Arg Arg Glu Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

Q2100: 21  
Q2110: 18  
Q2120: PRT  
Q2130: Artificial Sequence

Q2200:  
Q2230: Description of the artificial sequence:CDR3 region

Q4000: 21  
Arg Arg Arg Glu Gly Ala Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 22

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 21

Arg Arg Arg Glu Gly Gly Ala Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 23

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 21

Arg Arg Arg Glu Gly Gly Gly Ala Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 24

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 24

Arg Arg Arg Glu Gly Gly Gly Tyr Ala Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 25

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 25

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Ala Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 26

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 26

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Ala Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 17

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 17

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Ala Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 18

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 18

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Ala Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 29

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 29

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg

1

5

10

15

Arg Arg

<210> 30

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 30

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg  
1 5 10 15

Arg Arg

<210> 31

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 31

Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg  
1 5 10 15

Arg Arg

<210> 32

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 32

Arg Arg Arg Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 33

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 33

Arg Arg Arg Glu Gly Glu Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 34

4211> 18

4212> PRT

4213> Artificial Sequence

4220>

4223> Description of the artificial sequence:CDR3 region

4400> 34

Arg Arg Arg Glu Gly Gly Glu Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 35

4211> 18

4212> PRT

4213> Artificial Sequence

4220>

4223> Description of the artificial sequence:CDR3 region

4400> 35

Arg Arg Arg Glu Gly Gly Gly Glu Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 36

4211> 18

4212> PRT

4213> Artificial Sequence

4220>

4223> Description of the artificial sequence:CDR3 region

4400> 36

Arg Arg Arg Glu Gly Gly Gly Tyr Glu Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 37

4211> 18

4212> PRT

4213> Artificial Sequence

4220>

4223> Description of the artificial sequence:CDR3 region

<40> 37

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Glu Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<21> 36

<21> 16

<21> PRT

<21> Artificial Sequence

<2>

<2> Description of the artificial sequence:CDR3 region

<40> 38

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Glu Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<21> 39

<21> 16

<21> PRT

<21> Artificial Sequence

<2>

<2> Description of the artificial sequence:CDR3 region

<40> 39

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Glu Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<21> 40

<21> 16

<21> PRT

<21> Artificial Sequence

<2>

<2> Description of the artificial sequence:CDR3 region

<40> 40

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Glu Phe Asp Arg  
1 5 10 15

Arg Arg

<21> 41

<21> 16

<21> PRT

<21> Artificial Sequence

<2>

<2> Description of the artificial sequence:CDR3 region

<400> 41

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Glu Asp Arg  
1 5 10 15

Arg Arg

<210> 42

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 42

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Glu Arg  
1 5 10 15

Arg Arg

<210> 43

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 43

Arg Arg Arg Gly Glu Tyr Gly Glu Tyr Trp Asn Gly Asp Phe Tyr Arg  
1 5 10 15

Arg Arg

<210> 44

<211> 13

<212> PPT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 44

Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val  
1 5 10

<210> 45

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 45

Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg  
1 5 10

4210 46  
4211 14  
4212 PRT  
4213 Artificial Sequence

4220  
4223 Description of the artificial sequence:CDR3 region

4400 46  
Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp  
1 5 10

4410 47  
4411 18  
4412 PRT  
4413 Artificial Sequence

4420  
4423 Description of the artificial sequence:CDR3 region

4430 47  
Glu Glu Glu Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu  
1 5 10 15

Glu Glu

4440 48  
4441 18  
4442 PFT  
4443 Artificial Sequence

4450  
4453 Description of the artificial sequence:CDR3 region

4460 48  
Arg Arg Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4470 49  
4471 18  
4472 PRT  
4473 Artificial Sequence

4480  
4483 Description of the artificial sequence:CDR3 region

4490 49  
Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg  
1 5 10 15

Arg Arg

4210> 50  
4211> 57  
4212> DNA  
4213> Artificial Sequence

4220>  
4221> Description of the artificial sequence:primer

4400> 50  
gctgcatga ctgcgggcc agcggccat gccsaggtg marctgcags agtcwgg 57

4211> 51  
4212> 56  
4213> DNA  
4214> Artificial Sequence

4221>  
4222> Description of the artificial sequence:primer

4411> 51  
gtatcgtaa ctgcggccca gccggccatg gccgaggtgc agcttcagga gtcagg 56

4211> 52  
4212> 56  
4213> DNA  
4214> Artificial Sequence

4222>  
4223> Description of the artificial sequence:primer

4400> 51  
gtatcgtaa ctgcggccca gccggccatg gccgatgtgc agcttcagga gtcagg 56

4210> 53  
4211> 56  
4212> DNA  
4213> Artificial Sequence

4223>  
4224> Description of the artificial sequence:primer

4400> 53  
gtatcgtaa ctgcggccca gccggccatg gccaggtgc agctgaagsa gtcagg 56

4210> 54  
4211> 56  
4212> DNA  
4213> Artificial Sequence

4224>  
4225> Description of the artificial sequence:primer

4400> 54  
gtatcgtaa ctgcggccca gccggccatg gccaggtgc agctgcarca rtctgg 56

4211> 55

<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccaggttc arctgcagca gctcgg 56

<210> 5'  
<211> 5'  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccaggtga agctggtgga rctcgg 56

<210> 5'  
<211> 5'  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccaggttc agcttcagca gctcgg 56

<210> 5'  
<211> 5'  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccgaagtgc agctgktgga gwtcgg 56

<210> 5'  
<211> 5'  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccagatcc agttgctgca gctcgg 56

<210> 60  
<211> 60  
<212> DNA  
<213> Artificial Sequence

40000

4110 Description of the artificial sequence:primer

4111 61

atggtcagag ggcgcgccac ctgaaccgcc tccacctgag gagacggtga ccgtgggtccc 60  
atgggtccc 61

4112 61

4113 6

4114 DNA

4115 Artificial Sequence

42100

4211 Description of the artificial sequence:primer

4212 61

atggtcagag ggcgcgccac ctgaaccgcc tccacctgag gagacggtga ccgtgggtccc 60

4213 61

4214 6

4215 DNA

4216 Artificial Sequence

43100

4311 Description of the artificial sequence:primer

4312 61

atggtcagag ggcgcgccac ctgaaccgcc tccacctgag gagactgtga gagtgggtgcc 60

4313 60

4314 60

4315 DNA

4316 Artificial Sequence

44100

4411 Description of the artificial sequence:primer

4412 61

atggtcagag ggcgcgccac ctgaaccgcc tccacctgca gagacagtga ccagagtccc 60

4413 64

4414 60

4415 DNA

4416 Artificial Sequence

45100

4511 Description of the artificial sequence:primer

4512 64

atggtcagag ggcgcgccac ctgaaccgcc tccacctgag gagacggtga ctgagggttc 60

4513 66

4514 60

4515 DNA

4516 Artificial Sequence

46100

<223> Description of the artificial sequence:primer

<400> 65

tggtcagatg ggcgcgccctc tggcggtggc ggatcggaca ttgagctcac ccagtctcca 60

<210> 64

<211> 54

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 64

tggtcagatg ggcgcgccctc tggcggtggc ggatcggaca ttgtgatgac acagtctcc 59

<210> 67

<211> 54

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 67

tggtcagatg ggcgcgccctc tggcggtggc ggatcggatg tktgatgac ccaactcc 59

<210> 64

<211> 54

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 64

tggtcagatg ggcgcgccctc tggcggtggc ggatcggata ttgtgatrac ccaggcwg 59

<210> 64

<211> 54

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 64

tggtcagatg ggcgcgccctc tggcggtggc ggatcggaca ttgtgctgac ccactctcc 59

<210> 70

<211> 54

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 70

ggttcagatg ggcggcgctc tggcggtggc ggatcgaaaa wtgtctcac ccagtctcc 59

<210> 71

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 71

ggttcagatg ggcggcgctc tggcggtggc ggatcgaya tywgatgac mcagwctcc 59

<210> 71

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 71

ggttcagatg ggcggcgctc tggcggtggc ggatcgaaa ttgtctcac ccagtctcc 59

<210> 73

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 73

ggttcagatg ggcggcgctc tggcggtggc ggatcgcat tattgcaggt gcttggtgg 59

<210> 74

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 74

gaatcatct ggggacgccc gtttgatttc cagcttggtg cc 42

<210> 75

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 75

gagtcattct ggggacgccc gttttatttc cagcttggtc cc 42

<210> 76  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:primer

<401> 76  
agtcattct ggggcggccc gttttatttc cagtctggtc cc 42

<210> 77  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:primer

<401> 77  
agtcattct ggggcggccc gttttatttc caactttgtc cc 42

<210> 74  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:primer

<401> 74  
agtcattct ggggcggccc gtttcagctc cagcttggtc cc 42

<210> 79  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:mychis 6

<401> 74  
gggcgcagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60  
taataactaa taag 74

<210> 80  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:mychis

<401> 80  
gatttttatt agtgatggtg atggatgatgt gcgcgcccat tcagatcttc ttctgagatg 60  
agtttttggg ctgc 74

<210> 81

<211> 726  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 61  
 gaggagaagg tggaggagtc tggacotgag ctgaagaagg ctggagagac agtcaagato 60  
 ttttcaaggg cttttgggta tatcttcaca aactatggaa tgaactgggt gaagcaggct 120  
 ccagaaaagg gtttaaagtg gatgggttgg ataaacacot acaactggaga gccaacatat 180  
 tctgatgact tcaagggaag gtttgccttc tctttggaaa cctctggcag caatgcctat 240  
 ttgatgaca acaactcaca aaatgaggac acggctacat atttctgtgc attatatggt 300  
 aactcccta aggggtttgc ttactggggc caagggaact tggtcactgc ctctgcaggt 360  
 ggaggcgggt caggtggggc cgcctctggc ggtgggggat cggatattca gatgacacag 420  
 tctccaaat tctgtctgt atcagcagga gacagggta ccataacct caaggccagt 480  
 cagagtgtga gtaatgatgt agcttggtag caacagaagg cggggcagtc tctaaacta 540  
 cggatgact atgcatcaca tggctacact ggagtcctg atcgcttcac tggcagtgga 600  
 tatgggaagg atttcacttt caccatcagg actgtgcagg ctgaagacot ggcagtttat 660  
 tctctcaga aggattatgg ctctctctcc acgttcggag ggggcaccaa gctggaaatt 720  
 aaacgg 726

<410> 82  
 <411> 842  
 <412> PRT  
 <413> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 82  
 Gln Val Lys Leu Val Gln Ser Gly Pro Gln Leu Lys Lys Pro Gly Gln  
 1 5 10 15  
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr  
 20 25 30  
 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
 35 40 45  
 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Pro Thr Tyr Ala Asp Asp Phe  
 50 55 60  
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
 85 90 95  
 Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Arg Ala  
 115 120 125  
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe  
 130 135 140  
 Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser  
 145 150 155 160  
 Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln

165

170

175

Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val  
160 165 190

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr  
195 200 205

Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln  
210 215 220

Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
225 230 235 240

Lys Arg

<110> 83

<111> 747

<112> DNA

<113> Artificial Sequence

<120>

<121> Description of the artificial sequence:scFv region

<400> 83

taagtgacgc tgggtggagtc tggggggaggc ctagtgaagc ctggagggtc cctgaaactc 60  
tctctgtgcag cctctggatt cactttcagt acctatacca tgtcttgggt tggcagact 120  
tgggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagtta cactactat 180  
tcagacagtg tgaggggacg attcaccatc tcagagaca atgccaagaa cactctgtac 240  
atgcaaatga gcagcttgaa gtctgaggac acagccatgt attactgtac aagagatggg 300  
gacacggggt aggttagtag ctttgactac tggggccaag gcaccactct cacagtctcc 360  
tcagttggag ggggttcagg tggggcgggc tctggggtg ggggatgca aattgtgctc 420  
acccagttcc cactctccct gcctgtcagt cttggagtc aagctctcat ctcttgacga 480  
ctctgtcaga gcattgtaca tagtaatgga aacacctatt tagaatggta cctgcagaaa 540  
tcaggccagt ctccaaagct cctgatctac aaagtctcca accgattctc tggggctccc 600  
gacaaattca gtggcagtggt atcagggaca gatttcacac tcaagatcag cagagtggag 660  
cttgagggac tgggagtata ttactgcttt caaggttcac atgttcctgt gacgttcggg 720  
gagtgaccca agctggaaat caaacgg 747

<110> 84

<111> 249

<112> PRT

<113> Artificial Sequence

<120>

<121> Description of the artificial sequence:scFv region

<400> 84

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr  
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val  
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Ser Ser Leu Lys Ser Gln Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95  
 Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro  
 130 135 140  
 Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg  
 145 150 155 160  
 Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp  
 165 170 175  
 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val  
 180 185 190  
 Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser  
 195 200 205  
 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu  
 210 215 220  
 Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly  
 225 230 235 240  
 Gly Gly Thr Lys Leu Glu Ile Lys Arg  
 245

4110 - 65

4111 - 747

4112 - DNA

4113 - Artificial Sequence

4114 -

4115 - Description of the artificial sequence: scFv region

4116 - 65

gaggtagcagc ttcaggagtc aggggggagc ttagtgaagc ctggagggtc cctgaaaactc 60  
 tctgtgcag cctctggatc cactttcagt agctatacca tgtcttgggt tgcacagact 120  
 caggagaaga ggtggagtg ggtgcacacc attagtagtg gtggtagttc cactactat 180  
 ccagccagtg tgaagggtcg attcaccatc tcacagagaca atgccaagaa caccctgtac 240  
 ctgcacatga gcagtcctgag gtccgaggac acagccatgt attactgtac aagagagggg 300  
 gctgttttca ccgtcaactg gtacttcgat gtctggggcg cagggaactct ggtcactgtc 360  
 tctgcaggtg gaggcgggtc aggtggggcg gcctctggcg gtggcggatc ggaaaatgtg 420  
 ctcccccagt ctcagcttc tttggctgtg tctctaggcg agagggccac catatcctgc 480  
 adagccagtg aaagtgttga tagttatggt tataatttta tgcactggta tcagcagata 540  
 ccagacagc caccocaaact cctcatctat cgtgcaccca acctagagtc tgggatccct 600  
 ccagtggttca gtgcagtggt gtctaggaca gaattcacc tcaccattaa cctgtgtggg 660  
 gtgtgatgtg ttgcaacctt ttactgtcag caaagtaaty aggatccgct cactgttcgt 720  
 actggaacca gactggaaat aaaacgg 747

4110 - 66

4111 - 249

<212> 587

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region.

<400> 66

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Thr Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp  
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly  
115 120 125

Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser  
130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys  
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp  
165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala  
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser  
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val  
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly  
225 230 235 240

Thr Gly Thr Arg Leu Glu Ile Lys Arg  
245

<210> 67

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 87

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gaggtgacgc ttcaggagtc agggggaggg ttagtgaagc ctggagggtc cctgaaaactc 60
tcctgtgcag cctctggatt cttttttagt agttatacca tgccttgggt tcgccagact 120
ccggagaaga ggtctggagt ggtcgaaacc attagtagtg gtggtagttc cactactat 180
ccagacagtg tgaagggcgc attcaaccat tccagagaca atgccaagaa caccctgtac 240
ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcaatgtac aagagagggg 300
gtgtgttatt acgtcaactg gtacttccat gtctggggcg caggaccacac tctcacagtc 360
tcctcaggtg gaggcgggtc aggtggggcg gctctggcg gtgggggac ggacattgag 420
ctcacncagt ctccagcttc ttggctgtg tctctagggc agagggccac catatcctgc 480
agagtcagtg aaagtgttga tagttatggc aagagtttta tgcactggta ccagcagaaa 540
ccagggcagc caccctaaact cctcatctat cgtgcaccca acctagaata tgggatccct 600
gcaagttca gtggcagtg gtctaggaca gacttcaccc tcaccattaa tctgtggag 660
gtgatgatg ttgcnacota ttactgtcag caaagtaatg aggatccct caggttcgg 720
gttgagacca gactggaaat aaaacgg 747
```

<400> 88

<400> 249

<400> PRT

<400> Artificial Sequence

<400>

<400> Description of the artificial sequence: scFv region

<400> 88

```
Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
  1             5             10             15
```

```
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
      20             25             30
```

```
Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
      35             40             45
```

```
Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
      50             55             60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
      65             70             75             80
```

```
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
      85             90             95
```

```
Thr Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp
      100            105            110
```

```
Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly
      115            120            125
```

```
Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
      130            135            140
```

```
Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
      145            150            155            160
```

```
Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp
      165            170            175
```

```
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
      180            185            190
```

```
Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
```

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val  
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly  
225 230 235 240

Ala Gly Thr Arg Leu Glu Ile Lys Arg  
245

4110-69

4111-2199

4112-DNA

4113-Artificial Sequence

4120-

4123-Description of the artificial sequence:scFv region

4400-89

```

atgaaatacc tatttactac ggcagcgcct gaattgttat taactccggc ccagcccgcc 60
atggcgaggg tgaagcttgt aggtctctgg gaaggcttag tgaagcctgg agggctccctg 120
aaactctctc ttgcagcctc tggatttact ttccagtact ataccatgct ttgggttctg 180
agactctggg agaapaggtt ggaattgggt gaaacatta gtagtggngg tagttctacc 240
taattctcag acagtgtgaa gggcgccttc acatctctca gagacaatgc caagaatacc 300
ctgtacatgc aaatpaggag tctgaggtct gaggacacag ccatgtatta ctgtacacga 360
aggggggggtg gtttaccctt aaactgctac ttccatgtct gggcgcaggg aactcagtc 420
accgtctctc caggtgaggg cgggtccaggt gggcgcaggt ctgggggttg cggatccggc 480
attctgtctg cacagctctc agcttctctg gctgtgtctc tagggcagag ggcacacata 540
tccctgcagag ccagtgaag tgttcatagt tatggctata atttctgca ctggctaccg 600
tagtatccag gacagccac caaactctc atctatcttg catccaact agagtctcgg 660
atccctgcca ggttccagtg cagtgggtct aggcacagct tccacctac cattaatct 720
ctggaggtct atgatgttc aacctattac tctcagcaaa gtaattgagg taacctcacc 780
ttgggtactg gacacagct ggaataaaaa cgggcggcgg cagcccgggc accagaaat 840
cctgttcttg aaaaaccggc tgcctcaggg gatattactg caccgcggcg tctctcggc 900
ttaaagggtg atcagactgc cgtctctgct gattctctta cggataaacc tgcataaaat 960
attatcttgc tgattggcga tgggatgggg gactcggaaa ctactggcgc agctaattat 1020
gcccgaagtg cgggcggctt ttttaaaagt atagatgctt taacgcttac cgggcaatat 1080
actcaactat cgttgaataa aaaaaccggc aaacccgact accccaacca ctgggtctga 1140
tcagcaaccg cctgttcaac cgggttcaaa acctataacg ccgcgctggg ctctgatata 1200
tcagcaaaag atcaaccaac gattctggaa atggcaaaag ccgcaggtct agcgaccgt 1260
aacgttctta ccgcagagtt gcaggatgac acccccgctg cgtgtgtgga acatgtgaca 1320
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ggcggcggtg caaaaaacct tcttgaaaac gaaacggctg ctgaatggca gggaaaaacg 1500
ctgggtgaac aggcacaggg cgttggttat cagtgtgta gogatctgca tccactgaat 1560
tcgggtgagg aagcgaatca gaaaaaaccc ctgtttggac tgtttgctga cggcaatatg 1620
ctagtctgct ggttaggacc gaaagcaacg taactatgga atatcaataa gcccgcagtc 1680
acctgtacgc caaatccgca accgaatgac agtgtaccaa cctggcgca gatgacggac 1740
aaagcatttg aattgttgat taaaaatgag aaaggtttt tccctgaagt tgaaggtgag 1800
tcaatcgata aabagatca tcttgagaat ccttctgggc aaattggcga gaagtctgat 1860
ctcgtgaaag cgttacaacg ggcgtggaa ttogtataaa aggaggtata caggttggtc 1920
atactcaacg ctgatacgc ccacgcagc cagattgttg cgcgggatac caaanctccg 1980
ggctcaccac aggcgtataa taccaaaagt ggcgcagtga tgggtgatga ttacgggaac 2040
tcggaagagg attcacaaga acataccggc agtcagttgc gtattgggc gtatggcccg 2100
catgcgca atgttgttgg actgacggac cagaccgata tcttctacac catgaaagcc 2160
gtcttggggg atatgcaca ccatacccat caccattaa 2199

```

4210-91

4211-731

4212-PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 90

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly  
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu  
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr  
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp  
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn  
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser  
130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp  
145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln  
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly  
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys  
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg  
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro  
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu  
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala  
260 265 270

Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala  
275 280 285

Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp  
290 295 300

Gln	Thr	Ala	Ala	Leu	Arg	Asp	Ser	Leu	Ser	Asp	Lys	Pro	Ala	Lys	Asn	305	310	315	320
Ile	Ile	Leu	Leu	Ile	Gly	Asp	Gly	Met	Gly	Asp	Ser	Glu	Ile	Thr	Ala	325	330	335	335
Ala	Arg	Asn	Tyr	Ala	Glu	Gly	Ala	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	340	345	350	350
Ala	Leu	Pro	Leu	Thr	Gly	Gln	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	355	360	365	365
Thr	Gly	Lys	Pro	Asp	Tyr	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	370	375	380	380
Trp	Ser	Thr	Gly	Val	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	385	390	395	400
His	Glu	Lys	Asp	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	Lys	Ala	Ala	Gly	405	410	415	415
Leu	Ala	Thr	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	Thr	Pro	420	425	430	430
Ala	Ala	Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	Pro	Ser	435	440	445	445
Ala	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	Gly	Lys	450	455	460	460
Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	Thr	Leu	465	470	475	480
Gly	Gly	Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	Glu	Trp	485	490	495	495
Gln	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	Gln	Leu	500	505	510	510
Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	Asn	Gln	Gln	515	520	525	525
Lys	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	Met	Pro	Val	Arg	Trp	530	535	540	540
Leu	Gly	Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	Ile	Asp	Lys	Pro	Ala	Val	545	550	555	560
Thr	Cys	Thr	Pro	Asn	Pro	Gln	Arg	Asn	Asp	Ser	Val	Pro	Thr	Leu	Ala	565	570	575	575
Gln	Met	Thr	Asp	Lys	Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	Lys	Gly	580	585	590	590
Phe	Phe	Leu	Gln	Val	Glu	Gly	Ala	Ser	Ile	Asp	Lys	Gln	Asp	His	Ala	595	600	605	605
Ala	Asn	Pro	Cys	Gly	Gln	Ile	Gly	Glu	Thr	Val	Asp	Leu	Asp	Glu	Ala	610	615	620	620
Val	Gln	Arg	Ala	Leu	Glu	Phe	Ala	Lys	Lys	Glu	Gly	Asn	Thr	Leu	Val	625	630	635	640

Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp  
 648 650 655  
 Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala  
 660 665 670  
 Val Met Val Met Ser Tyr Gly Asn Ser Gln Glu Asp Ser Gln Glu His  
 675 680 685  
 Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn  
 690 695 700  
 Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala  
 705 710 715 720  
 Ala Leu Gly Asp Ile Ala His His His His His His  
 725 730

<110> 91

<111> 97\*

<112> DNA

<113> Artificial Sequence

<120>

<121> Description of the artificial sequence:scFv region

<400> 91

atgaaataacc tattgcttac ggcagccggt ggattgttat tactcgoggs ccagccggcc 60  
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 aaattctctt gtgcagcttc tggattcaact ttcaagtagct ataccatgts ttgggttcgs 180  
 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc 240  
 taccatccag acagtgtgaa ggcccgatcc accatctcca gagacaatgc caagaacacc 300  
 ctgtaccctgc aaatgagcag tctgaggtct gaggacacag ccattgtatta ctgtacaaga 360  
 aggggggggtg gtttcaacgt caactggtac ttcatgtctt ggggcgcagg aactccagtc 420  
 accgtctctt caggtggagg cggttcaggt gggcgcgctt ctggcggttg cggatcggac 480  
 attgtgtga cacagtntcc agcttctttg gtgtgtctc tagggcagag ggccaccata 540  
 tcttcagag ccagtgaag tgttgatagt tatggctata attttatgca ctggtatcag 600  
 cagataccag gacagccacc caaactcttc atctatctgt catccaacct agagtctggg 660  
 atctctgcca gtttcagtg cagtgggtct aggcagact tcaactccac cattaatctt 720  
 atgggggttg atgatgttgc aacctattac tgcagcaaaa gtaatgagga tccgctccag 780  
 tccgttactg ggcacagact ggaaataaaa cggcgggccg caccgaagcc ttccactccg 840  
 cccgggtctt cccgtatgaa acagctggaa gacaaagtag aggagctctt tagcaagaac 900  
 taccatctag aaaaagaggt agctcgtctg aaaaagctt ttggtgaacg tgggtggtac 960  
 catcaccttc accattaa 978

<110> 92

<111> 325

<112> PRT

<113> Artificial Sequence

<120>

<121> Description of the artificial sequence:scFv region

<400> 92

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
 1 5 10 15  
 Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly  
 20 25 30  
 Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu  
 50 55 60  
 Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr  
 65 70 75 80  
 Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
 85 90 95  
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp  
 100 105 110  
 Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn  
 115 120 125  
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser  
 130 135 140  
 Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp  
 145 150 155 160  
 Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln  
 165 170 175  
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly  
 180 185 190  
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys  
 195 200 205  
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg  
 210 215 220  
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro  
 225 230 235 240  
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu  
 245 250 255  
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala  
 260 265 270  
 Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln  
 275 280 285  
 Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu  
 290 295 300  
 Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His  
 305 310 315 320  
 His His His His His  
 325

<210> 93

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region.

<400> 23

```

atganatacc tattgootac ggcagcgcgt ggattgttat tactcggggc ccagccggcc 61
atgggacagg ttcagcttca gcagtctgga cctgagctgg tgaagccggg ggccctcagt 120
aagatttcct gcaaaagcttc tggctaagca ttcagtaact cttggatgaa ctgggtgaa 180
cagaaggctg gacagggctc tgaatggatt ggaaggattt atcctgaaa tggagatact 240
aactacaatg ggaagtcca gggcaaggcc acactgactg cagacaaatc cccagacaca 300
gootacatgc agctcagcag cctgacctct gtggaactct cgtctctctt ctgtgcagat 360
ggtaacctat attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 420
tcaggtggag ggggttcagg tggcgcgcc cctggcggtg ggggacgca aattgtcttc 480
accagctctc ctgcttcctt agctgtatct ctggggaga gggccacat ctcagtggg 540
gccaacaaa gtgtcagta atctggctat agttatatgc actggtacca acagaaacca 600
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aggttcagtg gcagtgggtc tgggacagac ttcacctca acatccatcc tgtggaggag 720
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gacacagctg cgtctctggt tgaattctct agcgataaac ctgcaaaaaa tattattct 960
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gacaccccaa cgtttctgga aatggcaaaa gcggcaggtc tggcgacggg taactgtct 1260
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gcaaaaaact ttgtgaaa ggaacogct ggtgaatggc agggaaaaa gctgtgtgaa 1500
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gaagcgaata agcaaaaaac cctgcttggc cgttttctg acggcaatat gcagtggtg 1620
tggctaggac cgaagcaac gtacatggc aatatogata agcccgagc cactctgac 1680
caaaatcggc aactgaatga cagtgtacca acctgggctg agatgacga caaagccatt 1740
gaattgttga gtaaaaaatg gaaaggtctt tctctgcaag ttgaaagtgc gtcactgat 1800
aaacaggatc atgttgogaa tcttggggg caaattggcg agacggtoga tctcgatgaa 1860
gcgtgacaa gggcgctgga attcgtcaaa aaggagggtc acacgtggt catagtcaac 1920
gttgatcaac cccacggcag ccagattgtt ggcgggata ccaagctcc gggcctcacc 1980
cagcgctcaa atacaaaag tgggcagtg atgtgatga gttacgggaa ctccgaagag 2040
gattacaaag aacatacggc cagtcagttg cgtattggcg cgtatggccc gaatgcggcc 2100
aatgtgtgtg gactgacga ccagacogat ctctctaca ccagtgaagg cgtctggtg 2160
gatatggac accatcaca tcaacattaa 2190

```

<211> 94

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 24

```

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
  1             5             10             15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
          20             25             30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
          35             40             45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
          50             55             60

```

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr  
 65 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys  
 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp  
 100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met  
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly  
 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu  
 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr  
 165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr  
 180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile  
 195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly  
 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu  
 225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg  
 245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ala  
 260 265 270

Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp  
 275 280 285

Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala  
 290 295 300

Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu  
 305 310 315 320

Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn  
 325 330 335

Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro  
 340 345 350

Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys  
 355 360 365

Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr  
 370 375 380

Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys  
 385 390 395 400

Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr  
 405 410 415  
 Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu  
 420 425 430  
 Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser  
 435 440 445  
 Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile  
 450 455 460  
 Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly  
 465 470 475 480  
 Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys  
 485 490 495  
 Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp  
 500 505 510  
 Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu  
 515 520 525  
 Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro  
 530 535 540  
 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr  
 545 550 555 560  
 Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr  
 565 570 575  
 Asp Lys Ala Ile Gln Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu  
 580 585 590  
 Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro  
 595 600 605  
 Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg  
 610 615 620  
 Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr  
 625 630 635 640  
 Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala  
 645 650 655  
 Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val  
 660 665 670  
 Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser  
 675 680 685  
 Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly  
 690 695 700  
 Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly  
 705 710 715 720  
 Asp Ile Ala His His His His His His  
 725

<210> 95  
 <211> 969  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 95  
 atgaatatac tattgcaatc ggcagccgct ggattgttat tactcgcgcc ccagccggcc 60  
 atgg ggagg ttcagcttca gcaatctgga cctgagctgg tgaagccggg ggccctcagt 120  
 agatattctt gcaaaagcttc tggctacgca ttcagtatct cttggatgaa ctgggtgaag 180  
 agagagcttg gacagggctt tgaatggatt ggaaggattt atctgggaaa tggagatact 240  
 aactcaatg ggaagtcca gggbaaggcc acactgactg cagacaaatc ctccagcaca 300  
 gcttcctg agctcagcag cctgacctct gtggactctg cggctctatt ctgtgcagat 360  
 ggtaagctat attactatgc tatggactac tggggccaag gaaactcagt cagcgtctcc 420  
 tcaggtggag ggggttcagg tggcgcgcc cctggcggtg ggggacgca aattgttctc 480  
 acccagcttc ctgcttctct agctgtatct ctggggcaga gggcaccat ctcatgcag 540  
 gccacaaaaa gtgctagta atctggctat agttatatgc actggtacca acagaaaaca 600  
 ggacggccac ccaaaactct catctatctt gcatccaaac tagaatctgg ggtccctgpc 660  
 aggtcagtg gcaatgggtc tgggacagac ttcacctca acatccatcc tgtggaggag 720  
 gaggatgctg caactatata ctgtcagcac agtagggagc ttcctgggac gttcggtgga 780  
 ggcacaaagg tggaaatcaa acggggcgcc gcacccaagg ctccactcc gcccggtct 840  
 tcccgtatga aacagctgga agacaaagta gaggagctcc ttggcaagaa ctaccatcta 900  
 gaaaacgagg tagctcgtct gaaaaagctt gttggtgaac gtggtggta ccatcaccat 960  
 cacccttaa 969

<210> 96  
 <211> 322  
 <212> FRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 96  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
 1 5 10 15  
 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Gln  
 20 25 30  
 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly  
 35 40 45  
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly  
 50 55 60  
 Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr  
 65 70 75 80  
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys  
 85 90 95  
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp  
 100 105 110  
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met  
 115 120 125  
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly

133	135	140
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu		
145	150	155 160
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr		
	165	170 175
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr		
	180	185 190
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile		
	195	200 205
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly		
	210	215 220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu		
	225	230 235 240
Ala Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg		
	245	250 255
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro		
	260	265 270
Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp		
	275	280 285
Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val		
	290	295 300
Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His		
	305	310 315 320
His His		

<110> 97  
 <111> 270  
 <112> DNA  
 <113> Artificial Sequence

<120>  
 <121> Description of the artificial sequence:scFv region

<110> 97  
 caggaaacag ctatgaccat gattacgcca agtttcacatg aaaatttat ttcaaggaga 60  
 cagtcataat gaaataccta ttgctaagg cagcgcctgg atgtttatta ctgcgggccc 120  
 acccggccat ggcccaggtg cagctgcagg cgggcctgca ggtcgacctc gagatcaaac 180  
 jggggggccc agaacaaaaa ctcatctcag aagaggatct gaatggggcg gcacatcac 240  
 atcaccatca ctaataagaa ttcactggcc 270

<110> 98  
 <111> 61  
 <112> PRT  
 <113> Artificial Sequence

<120>  
 <121> Description of the artificial sequence:scFv region

<400> 96

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val  
20 25 30

Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu  
35 40 45

Ala Asp Leu Asn Gly Ala Ala His His His His His His  
50 55 60

<400> 99

<111> 686

<111> DNA

<111> Artificial Sequence

<120>

<120> Description of the artificial sequence:scFv region

<400> 99

atgaatatac tattgctac ggcagccgct ggattgttat tactcgccgc ccagccggcc 60  
atgacccgag tgaagctggt ggagtctggg ggaggttag tgaagcctgg agggctccctg 120  
aaactccctt gtgcagcttc tggattcact ttcagtagct ataccatgtc ttgggttctg 180  
cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc 240  
tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc 300  
ctgtccctgc aaatgagcag tctgaggtct gaggacacag ccattgtatta ctgtacaaga 360  
gaggggggtg gtttcacagt caacttgtag ttgaggtct ggggggcagg aacctcagtc 420  
acgtctctct caggtggagg cgggttcaggt gggggcgct ctgggggtgg cggatcggac 480  
attatgctga cacagtctcc agctctcttg gctgtctctc tagggagag ggcaccata 540  
tcttgcagag ccagtgaag tcttgatagt tatggatata attttatgca ctggtatcag 600  
cagatccag gacagccacc caaactcttc atctatcgtg catccaacct agagtctggg 660  
atccctgcca ggttcagttg cagtgggtct aggcagact tcacctcac cattaatcct 720  
ctggaggctg atgatgttgc aacctattac tctcagcaaa gtaatgagga tccgtcacg 780  
tctgtactg ggaacagact ggaataaaaa cgggcggcgg cagaacaaaa actcatctca 840  
gaagaggctc tgaatggggc ggcacatcac catcaccata actaataa 888

<400> 100

<111> 294

<111> PRT

<111> Artificial Sequence

<120>

<120> Description of the artificial sequence:scFv region

<400> 100

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly  
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu  
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr  
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
                     85                    90                    95  
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp  
                     100                    105                    110  
 Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn  
                     115                    120                    125  
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser  
                     130                    135                    140  
 Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp  
                     145                    150                    155                    160  
 Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln  
                     165                    170                    175  
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly  
                     180                    185                    190  
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys  
                     195                    200                    205  
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg  
                     210                    215                    220  
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro  
                     225                    230                    235                    240  
 Val Gln Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu  
                     245                    250                    255  
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala  
                     260                    265                    270  
 Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
                     275                    280                    285  
 His His His His His His  
                     290

01100 101  
 01110 376  
 01120 DNA  
 01130 Artificial Sequence

01200  
 01230 Description of the artificial sequence: scFv region

04000 101  
 atgaaataac tattgcttac ggcagccggt ggattgttat tactggggg ccagccggcc 60  
 atggccggagg ttcagcttca ggcgtctgga cctgagctgg tgaagccgg ggccctcagt 120  
 atgatttcct gcaaaagcttc tggctacgca ttcagtagct cttggatgaa ctgggtgaag 180  
 cagaggccctg gacagggtct tgagtggatt ggaaggattt atcctggaaa tggagatact 240  
 aactacaatg ggaagttcaa gggcaaggcc aactgactg cagacaaatc ctccagcaca 300  
 gctacatgc agctcagcag cctgacctct gtggactctg cggctatatt ctgtgcagat 360  
 ggtaacgtat attactatgc tatggactac tgggtcaag gaacctcagt caccgtctcc 420  
 tcaggtggag ggggttcagg tggcgcgccc tctggcggtg ggggatcgca aattgttctc 480  
 acccagttct ctgcttcctt agtcttatct ctgggcgaga gggcaccat ctcatgcagg 540  
 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaaaca 600

ggacagccac scaaaactcct catctatctt gcatacaacc tagaatctgg ggtccctgac 660  
 aggttcagtg gcagtggggc tgggacagac ttcaccccca acatccatcc tggggaggag 720  
 gaggatgctg caacctatta ctgtcagcac agtagggagc ttccctggac gttcgggtga 780  
 ggcaccaagc tggaaatcaa acgggggggc gcagaacaaa aactcatctc agaagaggat 840  
 ctgaatgggg cggcacatca ccatacccat tactaa 876

<210> 102

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 102

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Ala
1			5						10					15
Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro
	20							25					30	
Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser
	35						40					45		
Tyr	Ala	Phe	Ser	Ser	Ser	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro
	50					55					60			
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Arg	Ile	Tyr	Pro	Gly	Asn	Gly	Asp
	65				70				75					80
Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp
			85						90					95
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Val
			100					105						110
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Asp	Gly	Asn	Val	Tyr	Tyr	Tyr	Ala
		115					120						125	
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly
	130					135					140			
Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val
145				150					155					160
Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala
			165					170						175
Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser	Val	Ser	Thr	Ser	Gly	Tyr	Ser
		180						185					190	
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Ile
		195				200						205		
Tyr	Leu	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser
	210					215					220			
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu
225				230						235				240
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Glu	Leu	Pro
			245						250					255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu  
 260 265 270

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His  
 275 280 285

His His His  
 290

<210> 103  
 <211> 74  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:primer

<400> 103  
 ggccacagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60  
 cactactaa taag 74

<210> 104  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:primer

<400> 104  
 ttattagtaga tggatgatggt gatgtgccgc cccattcaga tctctttctg agatgagttt 60  
 ttgttctgc 69

<210> 105  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:CDR3 region

<400> 105  
 Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys  
 1 5 10 15

<210> 106  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:CDR3 region

<400> 106  
 Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp  
 1 5 10 15